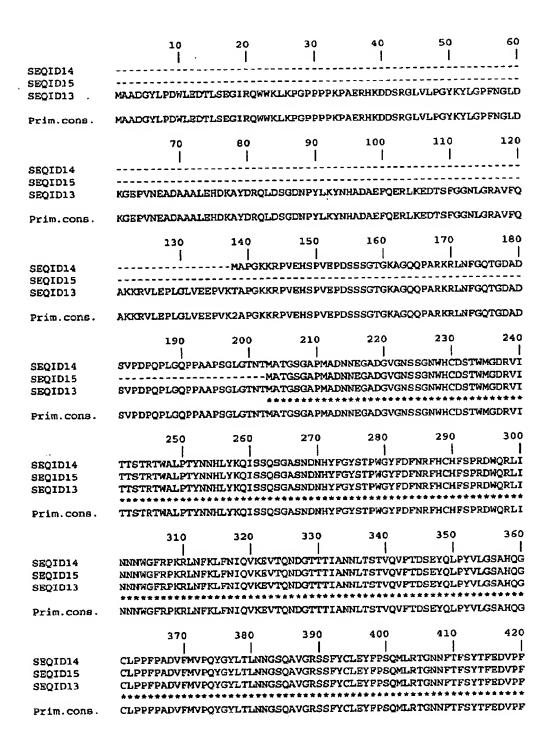
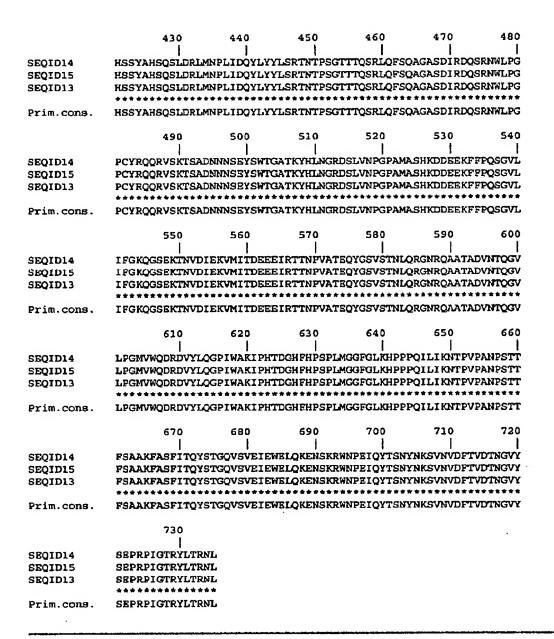
EXHIBIT B

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Alignment data: Alignment length: 735 Identity (*): 533 is 72.52 % Strongly similar (:): 0 is 0.00 % Weakly similar (.): 0 is 0.00 % Different: 202 is 27.48 %

Sequence 0001: SEQID14 (598 residues).VP2 Sequence 0002: SEQID15 (533 residues). VP3 Sequence 0003: SEQID13 (735 residues). VP1

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